QUALIFICATIONS AND TESTIMONIES

I have been developing DNA interpretation software since 1998 and am recognized as an expert, speaker, and instructor in the application and development of advanced DNA interpretation software.

My qualifications include authoring validations for software tools for kinship calculations, including deficiency cases, complex pedigrees, unidentified human remains, and incest cases. I have also authored peer-reviewed validations on probabilistic genotyping in semi-continuous and fully continuous models. I have authored laboratory analytical procedures for DNA interpretation, user training programs, and user manuals for DNA Interpretation software.

My opinions are based on my examination of the probabilistic genotyping results that were produced, as well as my training, education, experience, and expertise as a DNA interpretation software developer. My expert forensic opinions and the basis for those opinions are set forth more fully in this report and the DNA Case Review. (Exhibit 2) In addition, I am prepared to testify regarding the interpretation methods used to form my opinions, which were informed using external validation studies, internal validation studies, and scientific literature cited in the Procedures.

I did not track my expert testimonies before 2021, but prior years include admissibility hearings and direct testimony in Federal, Tribal, State, and County jurisdictions.

Curriculum Vitae, attached as Exhibit 1.

OVERVIEW

I prepared a report and conducted Probabilistic Genotyping on the reference and evidence samples provided.

DATA AND INFORMATION REVIEWED FOR THIS CASE

To form my opinions in this case, I reviewed the following materials:

DNA Reference profiles for Nicholas McGuffin and Leah Freeman and DNA evidence profile from Item 1.3 Right Shoe Cutting, Ankle were provided as raw genetic analyzer files in the ".hid" format provided by the Oregon State Police Forensic Services Division (OSP).

The documents reviewed include the Validation Study for STR Analysis, Volume 67—2016, portions of the Forensic Report dated October 10, 2017, and the associated Case File. The OSP STR Analysis Casework Procedures Manual dated 8/17/2017 and other tertiary documents and scientific literature have been cited.

BACKGROUND

Probabilistic genotyping is used in forensic DNA analysis to determine the likelihood that a certain set of DNA profiles originates from one or more individuals. It is a mathematically rigorous approach that considers the inherent uncertainty in DNA evidence and produces more accurate and reliable results than traditional binary methods for complex mixtures. This technique is commonly used in criminal investigations and has helped to solve many complex cases.

“Probabilistic genotyping refers to the use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios (LRs) and infer genotypes for the DNA typing results of forensic samples.” (SWGDAM, Guidelines for the Validation of Probabilistic Genotyping Systems, 2015)

Forensic laboratories face an increasing trend in the complexity of samples they are asked to analyze. Along with this trend, significant advancements in extraction methods, amplification chemistries, and CE instrumentation have improved sensitivity. However, these advancements have also posed a challenge in accurately resolving mixtures using binary mixture interpretation protocols. The previous methods used to evaluate low-level mixtures with allelic drop-in and drop-out using binary methods have proven insufficient.

The International Society for Forensic Genetics (ISFG) has published guidelines for interpreting low-level mixtures where dropout might occur (Gill et al., 2012). Sentry's Probabilistic Genotyping tool expands Dr. Peter Gill's research and includes the ability to analyze complex mixtures by factoring in "uncertainty."

Probabilistic Genotyping is a mathematically rigorous methodology free from bias. It determines the weight of evidence using a framework of competing hypotheses. However, analyzing the raw data for artifacts and determining the number of contributors to an evidence profile remains subjective and could lead to bias.

Sentry™ and STRMix™ are both fully continuous probabilistic genotyping software.

Sentry™ provides a high level of automation. The Maximum Likelihood approach is based on the frequentist inference, maximizing the likelihood function with respect to the unknown parameters to obtain the maximum likelihood estimate independently for competing hypotheses.

The software optimizes the Likelihood (under each hypothesis) as a function of the unknown parameters in the continuous model. The unknown parameters include:

Mix-Proportion: (mx1,…, mxC): mixture proportion for contributor 1,..,C.

PH Expectation: mean of a heterozygote peak height allele

PH Variability: coefficient of variance for a heterozygote peak height allele

Degradation: degradation slope

Stutter Prop: (n-1) and (n + 1) stutter proportions

Allelic drop-out

Allelic drop-in

Sentry™ uses the “exact method” for estimating genotypes with three unique models to determine the parameters that provide the best fit models. For these reasons, Sentry™ does not require laboratory-specific “training data sets.” The exact method makes Sentry™ completely laboratory, chemistry, and instrumentation agnostic.

In contrast, STRMix™ relies solely on Markov Chain Monte Carlo (MCMC) methodology to estimate genotypes and other unknown parameters. This limits the use of STRMix™ to laboratory-specific data based on laboratory chemistries and instrumentation.

I have run Sentry™ and STRMix™ in parallel for dozens of cases and have never observed divergent results wherein one software favors H_p versus H_d or vice versa. Both Sentry™ and STRMix™ have run diagnostic tools users are trained to use to determine if the results are reportable.

Probabilistic Genotyping is reliable and widely accepted in the scientific community. Sentry™ and STRMix™ are software tools implemented nationwide in multiple private and government forensic laboratories.

The Sentry™ and STRMix™ are programs that have been thoroughly validated in multiple Forensic DNA laboratories, including Genetic Technologies, Inc., before use in forensic casework.

The procedure for using these programs is developed using validation studies. I followed this procedure when using Sentry™ in this case. Another qualified forensic examiner reviewed and verified the reported Sentry™ results during the technical review process.

I could not use STRMix™ in this case due to the limitations presented when using MCMC methodology to estimate genotypes and other relevant parameters, requiring a laboratory-centric model maker. In New York vs. Hillary, John Buckleton analyzed NY OCME DNA evidence in STRMix™ without validating the NY OCME data models. For this reason, STRMix™ results were disallowed by the Court.

I, however, am qualified to review and opine on OSP STRMix™ results on all evidence samples where the STRMix™ run diagnostic pages are provided.

METHODOLOGY

The above-referenced evidence file was uploaded into GeneMapper IDX, which is used ubiquitously throughout the forensic human identification industry for genotyping raw analyzer files.

The evidence files were initially analyzed for baseline noise. The noise level was near 25 RFU across the overlayed dye lanes. To determine the sample-specific analytical threshold (AT) I took three standard deviations of the baseline noise. The value of 50

RFUs was calculated to be an appropriate analytical threshold for the evidence sample labeled Item 1.3 Right Shoe Cutting, Ankle.

The raw data files were “GeneMapped” at 50 RFUs using the GlobalFiler™ panel with the stutter filters turned on. Using the GeneMapper table export function, a table was created to include all discrete allele calls and their associated peak height intensities (RFU Values). This table was imported into Sentry ™ as an evidence file.

The evidence was assessed to determine the number of contributors (NoC). The NoC is inherently unknown and unknowable. Traditional methods consider allele counting and peak height ratios, coupled with analysts' experience.

Alternatively, or in conjunction with traditional methodologies for estimating the NoC, both Sentry™, and STRMix™ include tools to consider a range in a number of contributors and present the best-fit model. STRMix ™ uses a tool known as varNoC (variable number of contributors), and Sentry™ uses the AIC methodology (Akaike Information Criteria). For example, if an analyst could justify three or four contributors to a mixed evidence sample, they could use the PG software tools to run the range of three to four-contributor modules.

This is not the same as revisiting the NoC after examining the person of interest’s profile, say, by increasing the NoC and overall moderate uncertainty to support inclusion. (John S. Buckleton, Jo-Anne Bright, Simone Gittelson, & Tamyra R. Moretti, 2019)

The best-fit model for Item 1.3, Right Shoe Cutting, Ankle, (analyzed at 50 RFUs) was determined to support four contributors. The sample was scrutinized using traditional and software AIC methodologies. The evidence was slightly degraded, with a Degradation Slope of 0.84, which indicates that the smaller base pair-sized DNA fragments will survive over the larger fragments.

The Sentry™ AIC modeling tool favored a NoC of four with the degradation function turned, as seen below.

AIC Runs

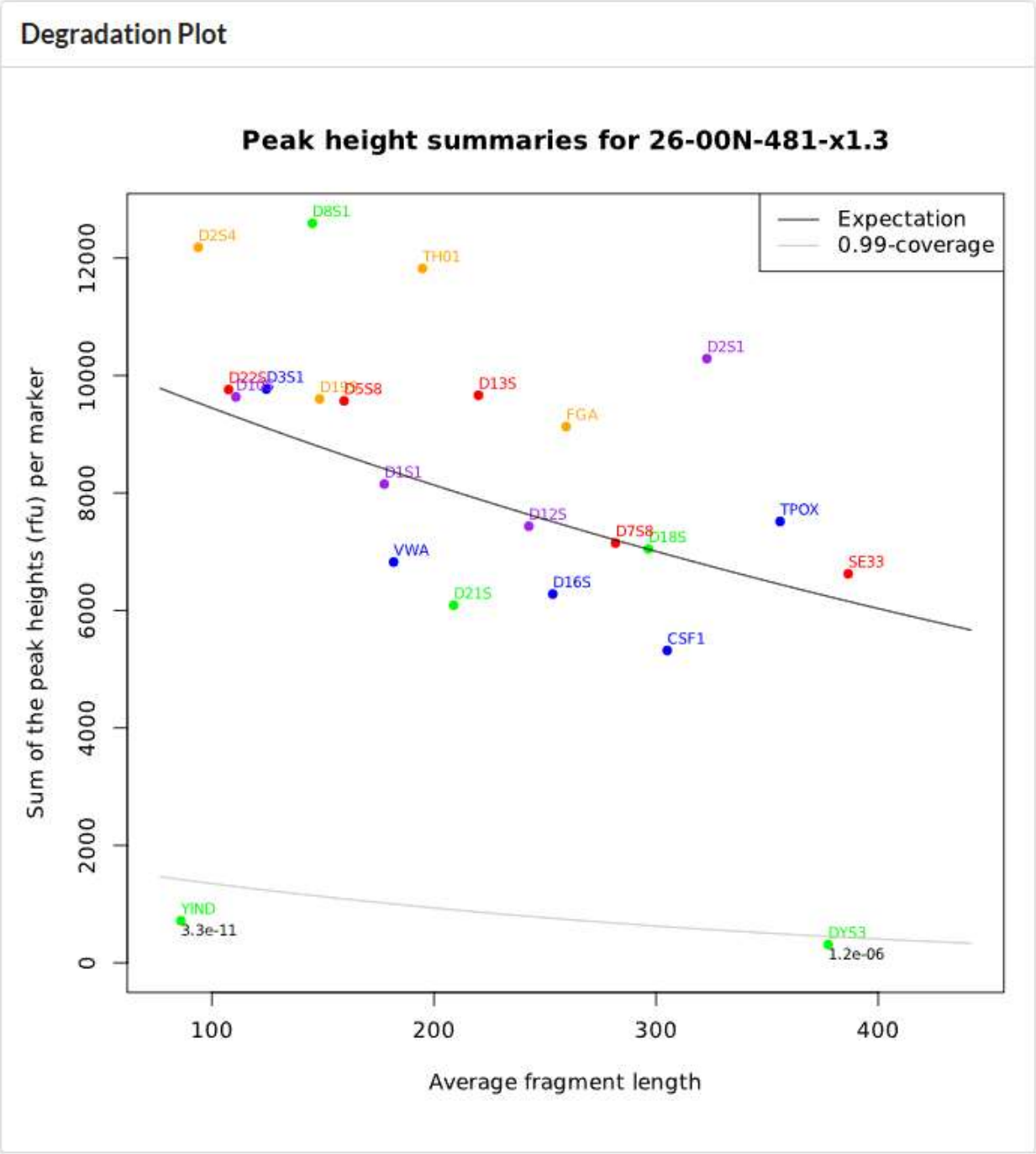
Show 10 entries

Number of Contributors	Use Degradation	Use Backward Stutter	Use Forward Stutter	logLik	AIC Score	log10LR	mxPOI	SignifHp	SignifHd
4	Yes	No	No	-768.5	-774.5	-3.21	0.015	0	0
4	No	No	No	-778.8	-783.8	-3.15	0.017	0	0
3	Yes	No	No	-792.0	-797.0	-28.11	0.022	6	0
3	No	No	No	-801.7	-805.7	-28.03	0.024	6	0

Showing 1 to 4 of 4 entries Previous 1 Next

Given the evidence degradation slope of 0.84, it was recognized that the DNA loci of the smaller base pair sizes may be more informative than those with larger fragment sizes,

especially considering the minor contributors. The degradation slope is depicted as follows:



The DNA reference profiles for Leah Freeman and Nicholas McGuffin were analyzed in GeneMapper IDX and uploaded into Sentry™.

Sentry™ calculates a likelihood ratio to provide a weight of evidence when comparing competing hypotheses documented as conclusions in my DNA Case Review, Exhibit 2. I will testify to the results found in this report and the supporting documentation that led to those conclusions.

The evidence was interrogated with competing hypotheses that independently calculated a likelihood. The H_p hypothesis questioned contributor Nicholas McGuffin, while assuming Leah Freeman, and two unknown, unrelated individuals. The H_d hypothesis questioned the assumed contributor Leah Freeman and three unknown, unrelated individuals.

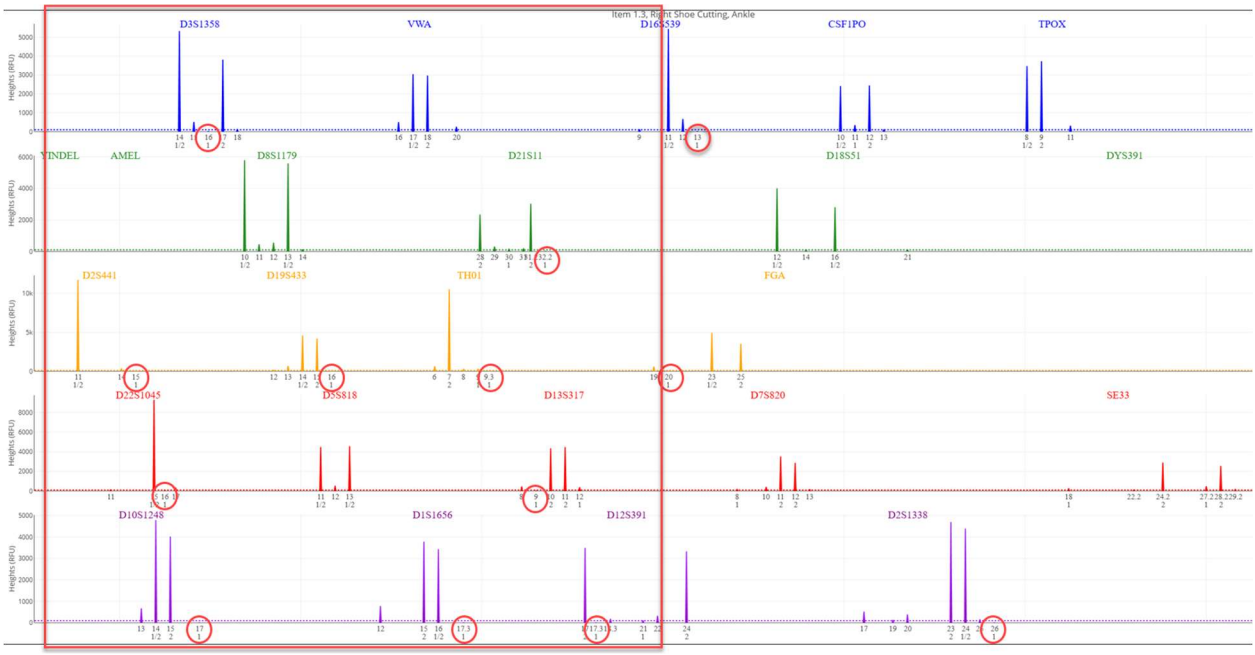
The weight of evidence is then expressed as a Likelihood Ratio (LR) by dividing the likelihood of H_p by the likelihood of H_d. A likelihood ratio greater than one favors H_p, while an LR less than one favors H_d.

The likelihood ratio was 0.0001484, much less than one, thus supporting the H_d hypothesis. The likelihood of 0.0001484 supports the exclusionary hypothesis.

It should be noted that I was asked to interrogate Item 1.3, Right Shoe Cutting, Ankle, for the presence of Nicholas McGuffin's DNA using the probabilistic genotyping methodology. However, I would have visually excluded McGuffin as a contributor to the evidence profile at the onset and performed no additional calculations.

The Scientific Working Group on DNA Mixtures (SWGDAM) states, "It would be inappropriate to make inclusions or exclusions based on the statistical approach without first considering the interpretation of the profile." (SWGDAM, 2021)

Based on earlier observations, DNA at loci at the smaller base pair sizes are less likely to "drop out," which indicates that the person of interest is excluded when obligate alleles are absent at these informative loci. The smaller base pair size loci are known as "minnies" and are identified in the red box overlay on the electropherogram (EPG) along with the absent obligate alleles belonging to McGuffin noted with red circles. This EPG is also in a larger format, as shown in Exhibit 3.

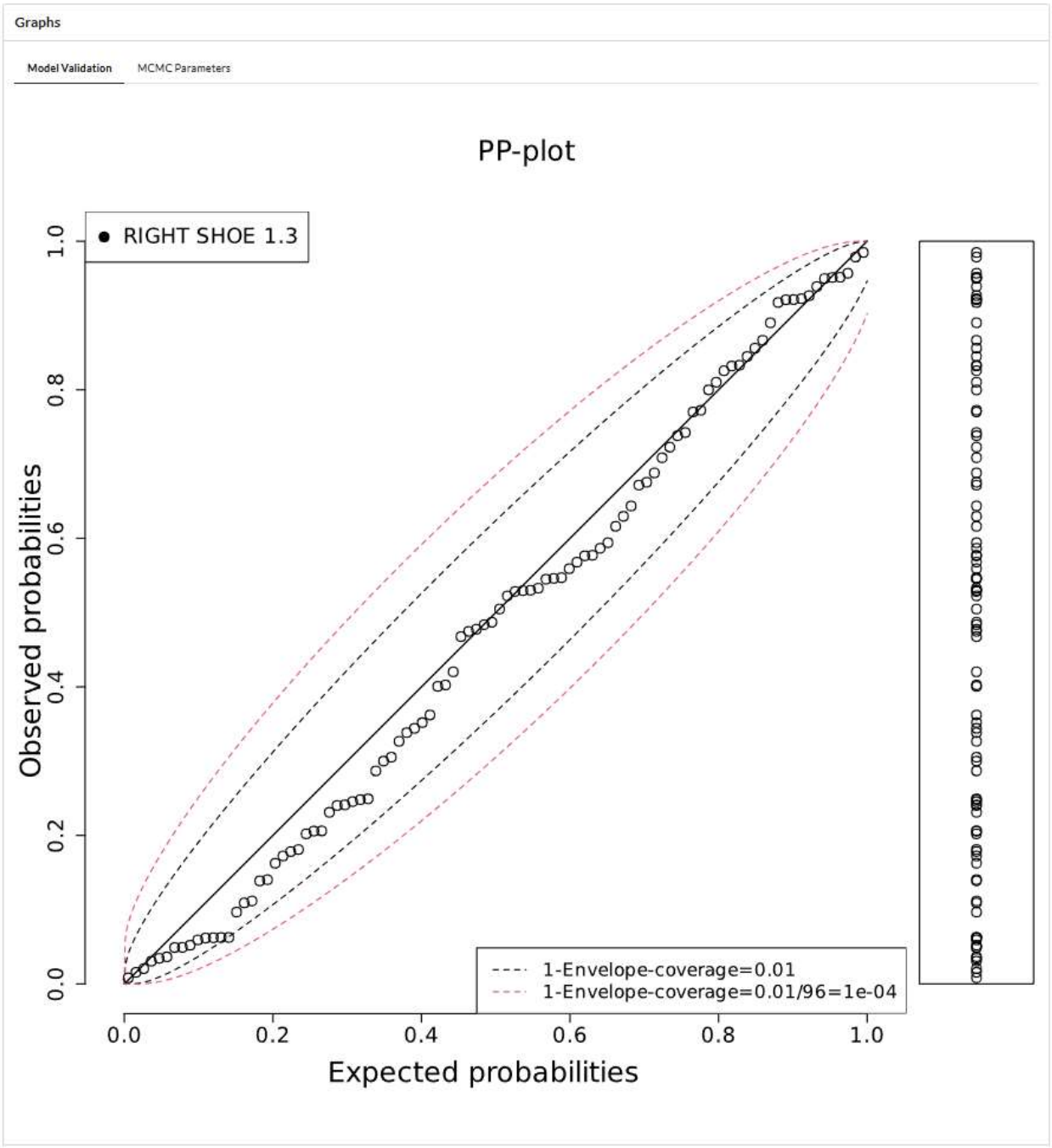


What follows and all probabilistic genotyping statistical calculations performed with McGuffin as a contributor to Item 1.3, Right Shoe Cutting, Ankle remain a moot exercise other than repeatedly demonstrating that all methods support the exclusion hypothesis.

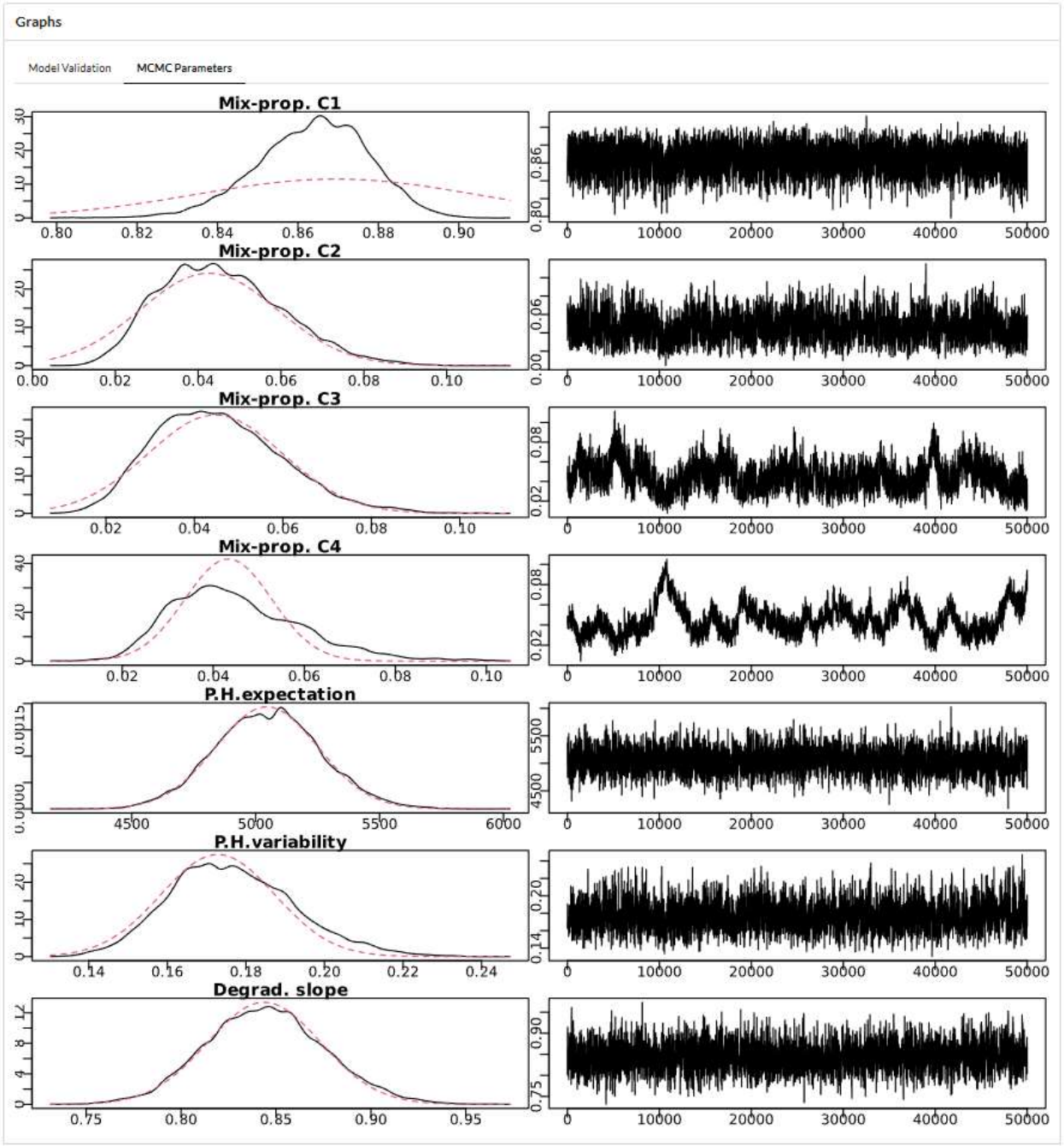
Sentry™ includes diagnostic tools to assess the validity of the hypotheses subjected to testing. The model consists of four contributors and a slightly degraded sample in this scenario.

Sentry™ validates these assumptions using Frequentist and Bayesian methodologies while calculating contributor Mixture Proportions, Peak Height Expectation, Peak Height Variability, and Degradation Slope."

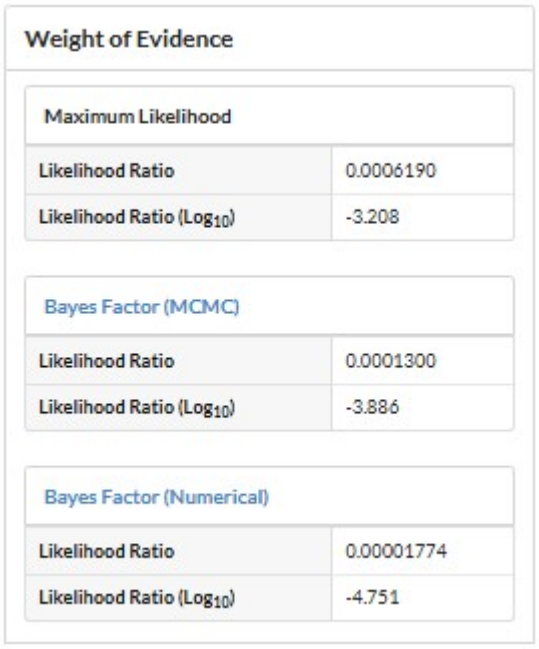
The Frequentist model validation graphic is presented as a PP-plot. The Bonferroni corrected significance level is set to a *narrow* 1% (0.01) and defines the PP Plot envelope. All points fall within the 1% significance level, thus demonstrating the "goodness of fit".



The Bayesian Model is an independent mathematical algorithm that implements the Markov Chain Monte Carlo (MCMC) simulation, assessing the model parameters' fit. The MCMC Simulation also demonstrates that the model selected is a good fit and that the parameter space was adequately explored.



It should be noted that Sentry™ results are run to run reproducible. Sentry™ used three mathematical models to assess the unknown parameters: Maximum Likelihood, Bayesian Factor (Numerical), and Bayes Factor (MCMC). All three methods converged, and the resulting likelihood ratios correspond below.



Weight of Evidence

Maximum Likelihood	
Likelihood Ratio	0.0006190
Likelihood Ratio (Log_{10})	-3.208

Bayes Factor (MCMC)	
Likelihood Ratio	0.0001300
Likelihood Ratio (Log_{10})	-3.886

Bayes Factor (Numerical)	
Likelihood Ratio	0.00001774
Likelihood Ratio (Log_{10})	-4.751

By assessing the run diagnostics, the user can determine that the mathematical models converged and that the observed probabilities closely track the expected probabilities.

This result would be reported as:

The DNA profile from Right Shoe 1.3 consists of a mixture of DNA.

Assuming four contributors and comparing the following hypotheses:

> H_p: 00N-481x1.3 Nicholas McGuffin, Leah Freeman 27-00N-481-x4, and two unknown, unrelated individuals
>
> H_d: Leah Freeman 27-00N-481-x4 and three unknown, unrelated individuals

It is 5.637E+04 (Fifty-Six Thousand Three Hundred Seventy) times more likely to obtain these results if Leah 27-00N-481-x4 and three unknown, unrelated individuals are contributors than if 00N-481x1.3 McGuffin, Leah 27-00N-481-x4, and two unknown, unrelated individuals are contributors. (Run 922)

Given that OSP ran both three- and four-contributor models for Item 1.3, Right Shoe Cutting, Ankle, I was also asked to run the three-contributor model. The three contributor results follow:

Assuming three contributors and comparing the following hypotheses:

> H_p: 00N-481x1.3 Nicholas McGuffin, Leah Freeman 27-00N-481-x4, and one unknown, unrelated individual
>
> H_d: Leah Freeman 27-00N-481-x4 and two unknown, unrelated individuals

It is 6.573E+28 (Sixty-Five Octillion Seven Hundred Thirty Septillion) times more likely to obtain these results if Leah 27-00N-481-x4 and two unknown, unrelated individuals are contributors than if 00N-481x1.3 McGuffin, Leah 27-00N-481-x4, and one unknown, unrelated individual are contributors. (Run 921).

The Scientific Working Group DNA Analysis Methods (SWGDAM) provides guidance on reporting genotyping results as likelihood ratios (SWGDAM, 2016).

The verbal qualifier for the four NoC model LR of 56,370 is Strong Support, and for the three NoC Model LR of 6.573E+28, it is Very Strong Support. This result confirms the earlier reported visual exclusion.

Please note that “Inconclusive” is not included in the SWGDAM verbal qualifier chart. (SWGDAM, Guidelines for the Validation of Probabilistic Genotyping Systems, 2015)

Table 1. **Scale of verbal qualifiers for reporting likelihood ratios**

LR **for** H_p **Support and 1/*LR*** **for** H_d **Support**	**Verbal Qualifier**
1	Uninformative
2 – 99	Limited Support
100 – 9,999	Moderate Support
10,000 – 999,999	Strong Support
≥1,000,000	Very Strong Support

STRMix™ diagnostics.

Like Sentry™, STRMix™ also includes run diagnostics that an analyst can use to determine if the evidence was modeled reliably. An LR | 1/LR in the range of ± 13,500 itself is not indicative of a failed probabilistic genotyping model, as the OSP contends. Coupled with passing diagnostics, it will provide a weight of evidence that should not be ignored. Again, “inconclusive” does not describe a probabilistic genotyping result.

OSP describes “inconclusive results” in section 16.10.5 in the OSP PROCEDURES MANUAL (2017)[1] as; “*Due to low levels of DNA, the limited DNA profile obtained from X (Exhibit X) is insufficient for comparison.”* This decision is made before analyzing for a “weight of evidence calculation” such as PG analysis.

[1] OSP PROCEDURES MANUAL (2017) was the version in use at the time of this OSP testing and analysis in this case.

Later in Section 16.12.10.J, titled “Inconclusive LR,” it is described: “*Individual A’s contribution to this DNA mixture is inconclusive. (S)he can neither be included nor excluded as a possible contributor.*”

In section 16.12.16, titled “Inconclusive mixture,” the OSP PROCEDURES MANUAL describes complex characteristics of the evidence profile, “*A [partial/limited] mixed DNA profile of at least XXX contributors [, including at least one male,] was obtained from X (Exhibit X). Due to low levels of DNA, the typing results are insufficient for comparison.*”. This assessment is made before further downstream analysis, such as PG, is attempted.

While using “inconclusive” to describe the evidence before PG analysis is acceptable and common, using “inconclusive” to describe PG results is not.

With that said, OSP uses a post-analysis probabilistic genotyping LR to determine if a result is inconclusive. Section 10.7.7.11 of their OSP PROCEDURES MANUAL describes the range of LRs under varying NoCs that will be labeled inconclusive. These post-analysis LRs are used even when the STRMix™ run diagnostics demonstrate reliable results. However, the OSP procedure directly opposes SWGDAM guidance, as referenced earlier.

If the number of contributors to the evidence profile is…	the person of interest cannot be excluded if LR is ≥	the person of interest is excluded if the LR is ≤
1	500 (5.00E+02)	0.00200 (2.00E-03)
2 or 3	2500 (2.50E+03)	0.000400 (4.00E-04)
4	13,500 (1.35E+04)	0.0000741 (7.41E-05)

The Oregon State Police acknowledges the STRMix™ diagnostic tools in their Validation Study for STR Analysis, Volume 67—2016, beginning on page 22, and in their 2016 OSP PROCEDURES MANUAL, beginning in section 10.6.2, page 92.

ESR, the developer of STRMix™, published a document titled, A guide to results and diagnostics within a STRmix™ report. (Russell L, 2019). In this peer-reviewed scientific journal, it explains, “A number of diagnostics have been included in the STRmix™ interpretation and are written to the report. They can be used to assess the results to ensure they are suitable for reporting.”

The STRMix™ diagnostics showed that the results from the PG analysis of Item 1.3, Right Shoe Cutting, Ankle, were reliable for the original run based on a NoC of 3. However, they later ran the same sample at a NoC of 4 with and without being conditioned on the victim. Exhibits 4-6

Oregon State Police reported results based on the four-contributor model.

To be clear, OSP initially ran this sample with a NoC of 3, and the run diagnostics showed the data was reliably modeled. It is unclear why they reran the same sample with a NoC of 4.

It should be noted that I analyzed the raw genetic data at a lower threshold (50) than the threshold used by the OSP (100). The lower threshold was used to better capture any low-level minor contributors. Therefore, when contrasted with the same data analyzed by OSP at a higher threshold, I identified additional alleles. The additional alleles would explain why my Sentry™ analysis favored a NoC of 4.

To further this assumption, I interrogated Nicholas McGuffin and Leah Freeman against Item 1.3, Right Shoe Cutting, Ankle, with an analytic threshold of 100 RFUs, the same as OSP implemented to analyze the data. At 100 RFUs, Sentry™ favored the model of three contributors. The results of the data analyzed at 100 RFUs are tabulated as follows:

Reference	Evidence	Com...	Total...	MAC	NoC	LR
00N-481x1.3 McGuffin	Item 1.3, Right Shoe Cutting, ...	21	42	0.69	3	1.228e-10
Leah 27-00N-481-x4	Item 1.3, Right Shoe Cutting, ...	21	42	1.0	3	7.786e+9

It should be noted that for the three-person model of evidence, data analyzed at 100 RFUs, the H_d hypothesis falls in the “Very Strong Support” range of LRs. In other words, the LR “very strongly supports” the exclusionary hypothesis.

I found no objective evidence as to why the OSP did not visually exclude McGuffin as a contributor or why they “shopped” the number of contributors in opposition to the STRMix™ software provider’s recommendations.

CONCLUSION

The OSP DNA tested Item 1.3, Right Shoe Cutting, Ankle, and several reference profiles for comparison.

I have unequivocally visually excluded Nicholas McGuffin as a contributor to Item 1.3, Right Shoe Cutting, Ankle. The follow-up probabilistic genotyping framework using competing hypotheses supports and confirms the visual exclusion.

However, the OSP remains equivocal and presents changing opinions, ultimately demonstrating egregious bias. Multiple reports have been issued with interpretations ranging from exclusion to inconclusive. Namely, the OSP's 2017 report that Mr. McGuffin's contribution is "inconclusive" regarding Item 1.3, Right Shoe Cutting, Ankle. This assessment is not supported by the data nor by professional and scientific standards.

The Amended Report dated May 17th, 2017, authored by Marla F. Kaplan, described Item 1.3, Right Shoe Cutting, Ankle, as a mixture of two, with a major female and minor male profile. The major profile was reported to match Leah Freeman.

Dennis Freeman, Nicholas McGuffin, Elzie Shamblin, Kip Oswald, William Sero, Unknown Male #1 (Exhibit 12.3), Unknown Male #3 (Exhibit 2.3), Unknown Male #4

(Exhibit 31.1) were excluded as possible contributors to the minor male profile in Item 1.3, Right Shoe Cutting, Ankle.

Four months later, OSP reanalyzed Item 1.3, Right Shoe Cutting, Ankle. During this analysis, the OSP used probabilistic genotyping, initially assuming three contributors and then later four contributors. To be clear, this evidence was reported as a mixture of two and later as a mixture of three and finally four contributors.

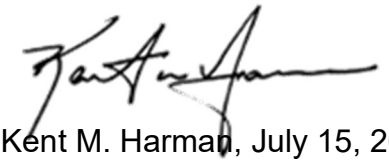
The most recent Analytical Report[2], dated October 10th, 2017, was authored by Janelle Moore and described Item 1.3, Right Shoe Cutting, Ankle, as a mixture of four, with Leah Freeman as the major profile.

The report then reads, “The contributions of Corey Courtright (Exhibit 9), Dennis Freeman (Exhibit 10), Nick McGuffin (Exhibit 13), Elzie Shamblin (Exhibit 45), Kip Oswald (Exhibit 47), William Sero (Exhibit 48), Brent Bartley (Exhibit 78), Randy Ulmer (Exhibit 79), Anthony Messarle (Exhibit 80), Ronald Robinson (Exhibit 81), Josh Emler (Exhibit 83), Aaron West (Exhibit 84), David Jenkins (Exhibit 85), Thomas Stemmerman (Exhibit 86), and Richard Crook (Exhibit 87) to this mixture are inconclusive. They can neither be included nor excluded as possible contributors.”

Inconclusive is not used to describe a probabilistic genotyping result (SWGDAM, 2016); furthermore, the phrase, “They can neither be included nor excluded as possible contributors,” is highly prejudicial. This statement insinuates that an individual could be included as a contributor, which is inaccurate according to OSP's own data.

Remember that Nicholas McGuffin is visually excluded as a contributor to Item 1.3, Right Shoe Cutting, Ankle, yet OSP chooses to perform probabilistic genotyping. They further exacerbate their predisposition by reporting an inconclusive result. Even though I have shown that “inconclusive” is not a verbal predicate used to describe a probabilistic genotyping LR, the OSP proceeded to compound their prejudice by summarizing, “They can neither be included nor excluded as possible contributors.” As fact, I do not accept their conclusion. However, the OSP could mitigate its pro-prosecution bias with a non-biased statement such as “Due to mixture complexity, no further interpretations can be made.”

Respectfully submitted,



Kent M. Harman, July 15, 2024

[2] Note: the report format violates Accreditation Standards on Amended Reporting (17025:2017) Exhibit 7

Works Cited

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Exhibit 1

Kent M. Harman

Objective: To familiarize colleagues with Kent M. Harman's business, scientific, and leadership experience.

I have successfully created Genetic Technologies, Inc. (GTI), a private forensic DNA testing laboratory. It was the first in the Midwest to implement advanced PCR and STR capillary electrophoresis technologies.

Grew GTI into a multi-accredited organization with a Nationwide footprint. Provided forensic biology testing, consultation, and DNA interpretation software as a service to government and private laboratories/agencies.

Successfully merged Genetic Technologies, Inc.'s forensic biology testing operation with Sorensen Forensics, LLC, two multi-accredited Forensic Biology laboratories. Served as Chief Executive Officer of the merged assets for four years. Restored Sorenson Forensics' reputation in the industry and positioned them for sustainable growth.

Implemented new training programs, analytical procedures, and a new quality assurance team, and implemented sophisticated software custom-designed for quality monitoring. Designed and oversaw the construction of the new customized laboratory in Draper, Utah.

I am fully experienced in forensic biology and relatedness testing using numerous CE/related platforms, kit chemistries, and qualified expert witness.

Experience:

Genetic Technologies, Inc.	St. Louis, Missouri
President & CEO	1998 to Present
Sorenson Forensics & GTI Merged Assets	Draper, Utah
CEO, Managing Member, and Owner	2018 to 2022
Sorenson Forensics LLC	Draper, Utah
Managing Member and Owner	2018 to Present

DNA Solutions, Inc. Oklahoma City, Oklahoma

Consulting General Manager January 2024 to Present

Experience Continued:

- Continue implementing new DNA services to diversify the laboratory's revenue base.
- Commissioned and oversaw the implementation of internal scientific validation studies.
- Commissioned and oversaw the implementation of a Laboratory Information Management System (LIMS) to streamline laboratory throughput and Quality Control.
- Commissioned and oversaw the implementation of Kinship algorithms and provided consultation with laboratories nationwide.
- Commissioned and oversaw the implementation of BP Sentry, a continuous probabilistic genotyping software widely used in forensic DNA laboratories.
- Frequently invited as a guest speaker/trainer by accredited laboratories and scientific organizations on Kinship Calculations, LIMS implementation, probabilistic genotyping calculations, and theory.
- Consultant to the Illinois State Police Laboratory System for matters concerning relatedness calculations involving remains identification and criminal paternity.
- Consultant and software provider to the Orange County District Attorney’s Office for matters concerning DNA Data Basing and Familial Searches in a criminal database.
- Commissioned and oversaw the implementation of Custom Developed Forensic LIMS Modules for U.S. Government Laboratories.
- Provide Forensic LIMS and Database Solutions through USAID—the latest successful implementation in Colombo, Sri Lanka.

- Commissioned and oversaw the implementation of software and tools for NetBio and ANDE Corporation Rapid DNA for disaster victim identification, familial searching, and complex kinship calculations.

- Commissioned and oversaw the implementation of BP Sentry, a specialized software designed to be used as a bulk repository for all DNA profiles, probabilistic searching for quality assurance, and a continuous model probabilistic genotyping and mixture deconvolution tool.

Education:

Fontbonne University Clayton, Missouri

Master's in Management

Fontbonne University Clayton, Missouri

Bachelor of Business Administration

Meramec College

Coursework to include Biology, Chemistry

Continuing Education, Training & Presentations

1998 Perkin Elmer – Applied Biosystems

310 Genetic Analyzer & AmpFISTR Training

1998 Perkin Elmer – Applied Biosystems

Missouri State Highway Patrol Criminal Laboratory
310 Genetic Analyzer User's Forum

1999 Midwestern Association of Forensic Scientists & Illinois State Police

Spring 1999 DNA STR Workshop

1999 Promega Corporation
10th International Symposium on Human Identification

1999 Promega Corporation
Statistics Workshop

1999 Perkin Elmer- Applied Biosystems
STR Forensic Meeting

2000 Promega Corporation
11th International Symposium on Human Identification

2000 Promega Corporation
11th International Symposium on Human Identification
Casework Guidelines & Complex Mixture Interpretation Workshop

2000 SWGDAM Meeting
11th International Symposium on Human Identification
(Scientific Working Group for DNA Analysis Method)

2001 SWGDAM Meeting
12th International Symposium on Human Identification
Scientific Working Group for DNA Analysis Methods

2001 Promega Corporation
12th International Symposium on Human Identification
Statistics and Mixture Interpretation Workshop

2002 Midwestern Association of Forensic Scientists
2002 STR Symposium

Mixture Issues and New Technology

2002 American Association of Blood Banks, 54th Annual Meeting

- Guest Speaker (LIMS)
- Parentage Testing Sig I
- Parentage Testing Sig II

2003 Promega Corporation

14th International Symposium on Human Identification

- Parentage Symposium
- Guest speaker on high throughput LIMS

2004 Sorensen Genomics

- Instructor in a relatedness statistics workshop
- Instructor in a LIMS QA/QC workshop
- Instructor in LIMS implementation

2005 Midwestern Association of Forensic Scientists

Fall 2005 – ASCLD/LAB Criteria File & ISO Workshop

2005 Midwestern Association of Forensic Scientists

Fall 2005 – Forensic Statistics Workshop

2006 Applied Biosystems – HID University

AB Product Updates: Allelic Ladder Manufacturing and

AmpF/STR® Yfiler™ PCR Amplification Kit

2006 Promega Corporation

17th International Symposium on Human Identification

Advanced Topics in Forensic Statistics

2006 Promega Corporation

17th International Symposium on Human Identification

Generating DNA Profiles from Difficult Samples

2007 Applied Biosystems – HID University

Future Trends in Forensic DNA Technology

2007 7500 Real-Time PCR

Training provided by Applied Biosystems regarding the qPCR chemistries and operational maintenance of the 7500 Real-Time qPCR Tower equipment.

2008 Applied Biosystems – HID University

Future Trends in Forensic DNA Technology

2008 Applied Biosystems – HID University

GeneMapper IDX – Discover the Next Generation

2008 MAFS

Integrity, Character and Ethics in Forensic Science

2008 MAFS

Workshop on Mixture Evaluation

2008 MAFS

Body Fluid Identification – New Techniques for Old Problems

2008 MAFS

Bloodstain Pattern Interpretation for DNA Analysts

2009 Ron Smith & Associates, Inc.

Courtroom Testimony Techniques: Success Instead of Survival

2010 Forensic Quality Services
Forensic Relationship Testing Workshop

2010 Federal Bureau of Investigation
Quality Assurance Standards Auditor Training

2011 Applied Biosystems HID University
Future Trends in Forensic DNA Technology

2011 Midwestern Association of Forensic Scientists
Y Not? Forensic Y-STR Testing

2011 Midwestern Association of Forensic Scientists
Forensic Relationship Statistics

2012 Promega Corporation
23rd International Symposium on Human Identification

2012 Promega Corporation
Y-STR Mixture Interpretation

2012 California Department of Justice / Criminalistics Institute
Population Genetics and Complex Kinship Statistics
Familial Searching and CODIS

2014 The Center for Advanced Forensic DNA Analysis
GenomeID Forum

Emerging Forensic Genomic Applications

2015 Probabilistic Genotyping

Caymans Forensic Science Laboratory

Dr. Norah Rudin and Keith Inman

2015 Illumina MiSeq FGx On-Site

Illumina, Inc. Presentation: Aimee Keithly, Sr. Account Manager

2015 RapidHit DNA On-Site

Integenex Presentation: Richard Brooks, Ph.D. & Dave Oehler

2015 Qiagen EZ1/Investigator Argus X-12 On-Site

Qiagen Training/Presentation: Dr. Meredith Turnbough, Ph.D. & Dr. Mark Guilliano, Ph.D.

2015 Illumina MiSeq FGx On-Site

Illumina, Inc. Presentation: Aimee Keithly, Sr. Account Manager, Ann Alison, Dr. Steven Lee

2016 Association of Forensic Analysts and Administrators

Current Forensic DNA Analysis Topics

2016 Scientific Collaboration, Innovation & Education Group

(SCIEG)

Likelihood Ratios & Probabilistic Genotyping Workshop

2017 Green Mountain DNA Conference

Subject Matter Expert / Presenter: Complex DNA Calculation

2017	Rapid DNA Technology Forum Forensic Technology Center of Excellence
2018	California Department of Justice / Criminalistics Institute R500 Kinship v2 (5-day course)
2018	ISHI 29 Forensic Software—Issues of Validation and Verification
2019	4th Annual National SAKI Grantees Meeting Washington D.C.
2019	ISHI 30 General Sessions
2019	ISHI 30 AABB Workshop as guest lecturer on complex DNA calculations
2019	ISHI 30 HITA Workshop – Are you Prepared for a Mass Fatality Incident Response?
2020	Federal Bureau of Investigation 7/20 Quality Assurance Standards Auditor Training
2020	ANDE Rapid DNA Onsite Rapid DNA Instrument Training provided by ANDE Corporation
2020	ThermoFisher – Life Technologies

Quant Studio 5 Training (Quant Trio and Virtual Curves)

2021 Applied Biosystems GeneMapper ID-X

Tips and Tricks from PeterGene: Uninhibited Ep. #6

2021 BP Sentry Probabilistic Genotyping Advance Users Workshop

2022 SWGDAM NGS Committee

Integration of Probabilistic Genotyping methodologies using LUS and LUS+ sequencing data formats for forensics and human identification.

2023 American Academy of Forensic Scientists

Presenter/speaker on improved Human Remains Identification DNA calculations compared to the widely used but incorrect Kinship Proxy.

2023 Probabilistic Genotyping Classroom Instruction

Instructor at the Vermont State Police Forensic DNA Laboratory: 40 hours of in-depth PG and DNA Interpretation training.

2023 Green Mountain DNA Conference

Burlington, Vermont

Presentation on Kinship vs. UHR calculations

2023 International Symposium of Human Identification (ISHI)

Denver, Colorado

TESTIMONY LIST[3]

2021 Daubert Hearing

State OK v Patrick Napoleon CF-2017-2208

[3] List does not include testimony prior to 2021

Tulsa, Oklahoma

2022 State vs. Jerrod Baum, Case No. 181401062
Utah County, Utah

2022 State vs. Eric Oliver
Memphis, Tennessee

2023 Probabilistic Genotyping Testimony
State OK v Patrick Napoleon CF-2017-2208
Tulsa, Oklahoma

2023 Complex Kinship Testimony (Incest calculations)
State of Utah vs. Scott Garza, Case Number: 211100360
Cache County, Utah

2024 Forensic Biology, Sexual Assault
US v CPL Marcus Mobley, US Army
7th Army Training Command, Vilseck, Bavaria

A practitioner with the following equipment, chemistries/reagents, and software. This list is not all-inclusive.

Equipment:

- Pipettes (various brands and types)
- Centrifuges (various brands and types)
- Alternate light source
- Fume and PCR Hoods
- Microscopes (various brands and types)
- Stereoscope
- Incubators (various brands and types)
- Thermoshakers (various brands and types)
- Qiagen EZ-1 Advanced XL Robotic DNA Extraction Platform
- Maxwell® Rapid Sample Concentrator 48

- Savant DNA SpeedVac Concentrator
- Qiagen Lyse & Spin Baskets
- Organic Extractions (Phenol chloroform)
- Zymo DNA Clean & Concentrator-5
- Phase Lock Gel tubes
- ABI 7500 Real-Time PCR Tower
- QuantStudio™ 5 Real-Time PCR SystemGeneAmp™ PCR System 9700
- 310, 3130, and 3500 Genetic Analyzers

Chemistries / Reagents:

- Acid Phosphatase / Brentamine Test (seminal fluid)
- SERATEC PSA (p30) Semiquant (seminal fluid)
- Christmas Tree Stain (microscopic sperm search)
- Phenolphthalein Test (blood)
- Luminol Test (blood)
- ABAcard® HemaTrace® (blood)
- Organic DNA extraction: stain extraction buffer, Proteinase K, Phenol-Chloroform-Isoamyl alcohol, TE Buffer, Dithiothreitol
- Zymo DNA Clean & Concentrator-5 kit
- Quantifiler Duo DNA Quantification Kit
- Quantifiler Tri DNA Quantification Kit
- PowerQuant System Kit
- Profiler Plus PCR Kit
- Identifiler PCR Kit
- Identifiler Plus PCR Kit
- Y-Filer PCR Kit
- Y-Filer Plus PCR Kit
- PowerPlex Y23 PCR Kit
- GlobalFiler PCR Kit
- Fusion 5C and 6C PCR Kits
- Spectral Matrix Standards for all PCR and qPCR kits
- Promega SwabSolution™ Kit
- Promega Casework Direct Kit

Forensic Biology Software:

- eDNA LIMS (with BRUTUS)
- Qualtrax (Quality & Document management)
- GeneScan
- Genotyper
- GeneMapper ID 3.2
- GeneMapper ID-X 1.4 through 1.7

- 7500 and QS5 HID RT Software
- EuroForMix (probabilistic genotyping)
- Sentry (probabilistic genotyping)
- STRMix (probabilistic genotyping)

Exhibit 2

DNA Case Review

Janis C. Puracal
Andrew C. Lauersdorf
Maloney Lauersdorf Reiner PC
1111 E. Burnside St., Suite 300
Portland, Oregon 97214

David B. Owens
Loevy & Loevy c/o
Civil Rights and Justice Clinic
University of Washington Law School
William H. Gates Hall, Suite 265
PO Box 85110
Seattle, WA 98145-1110

Nicholas McGuffin and S.M. v. Mark Dannels, et al.

Case Name(s) Leah Freeman - [Victim]
Nicholas McGuffin - [POI]

Review Summary

The undersigned reviewed data including raw genetic analyzer files for one piece of evidence and two reference profiles. The data was analyzed using GeneMapper IDX, and Probabilistic Genotyping statistics/weight of evidence were generated using Sentry™.

Summary of Findings

Nicholas McGuffin can be visually excluded as a contributor to Item 1.3, Right Shoe Cutting, Ankle.

Statistical analysis is not required for visual exclusions; however, the client requested probabilistic genotyping results based on the assumption of three and four contributors.

1. The DNA profile from Item 1.3, Right Shoe Cutting, Ankle consists of a mixture of DNA.

Assuming four contributors and comparing the following hypotheses:

Hp: 00N-481x1.3 McGuffin, Leah 27-00N-481-x4, and two unknown, unrelated individuals

Hd: Leah 27-00N-481-x4 and three unknown, unrelated individuals

It is 5.637E+04 (Fifty-Six Thousand Three Hundred Seventy) times more likely to obtain these results if Leah 27-00N-481-x4 and three unknown, unrelated individuals are contributors than if 00N-481x1.3 McGuffin, Leah 27-00N-481-x4, and two unknown, unrelated individuals are contributors. (Run 922)

2. The DNA profile from Item 1.3, Right Shoe Cutting, Ankle consists of a mixture of DNA.

Assuming three contributors and comparing the following hypotheses:

Hp: 00N-481x1.3 McGuffin, Leah 27-00N-481-x4, and one unknown, unrelated individual

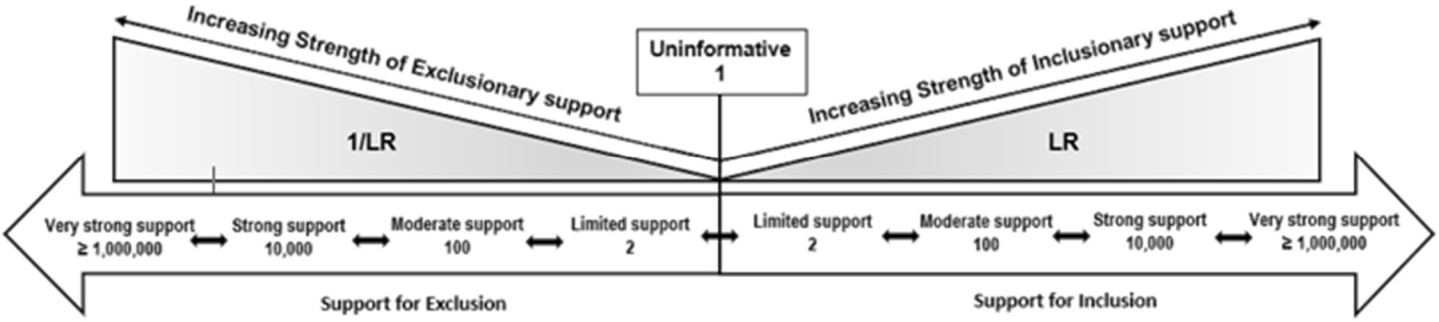
Hd: Leah 27-00N-481-x4 and two unknown, unrelated individuals

It is 6.573E+28 (Sixty-Five Octillion Seven Hundred Thirty Septillion) times more likely to obtain these results if Leah 27-00N-481-x4 and two unknown, unrelated individuals are contributors than if 00N-481x1.3 McGuffin, Leah 27-00N-481-x4, and one unknown, unrelated individual are contributors. (Run 921)

Notes:

The NIST General population data were obtained from NIST 1036 Revised U.S. Population Dataset (July 2017), retrieved from the National Institute of Standards and Technology STRbase on the World Wide Web: http://www.cstl.nist.gov/biotech/strbase/NISTpop.htm.

The SWGDAM verbal equivalents for numerical Likelihood Ratio (LR) designations are stated in the chart below.



Respectfully submitted,

Kent M Harman July 15rd 2024
Probabilistic Genotyping SME

Exhibit 3

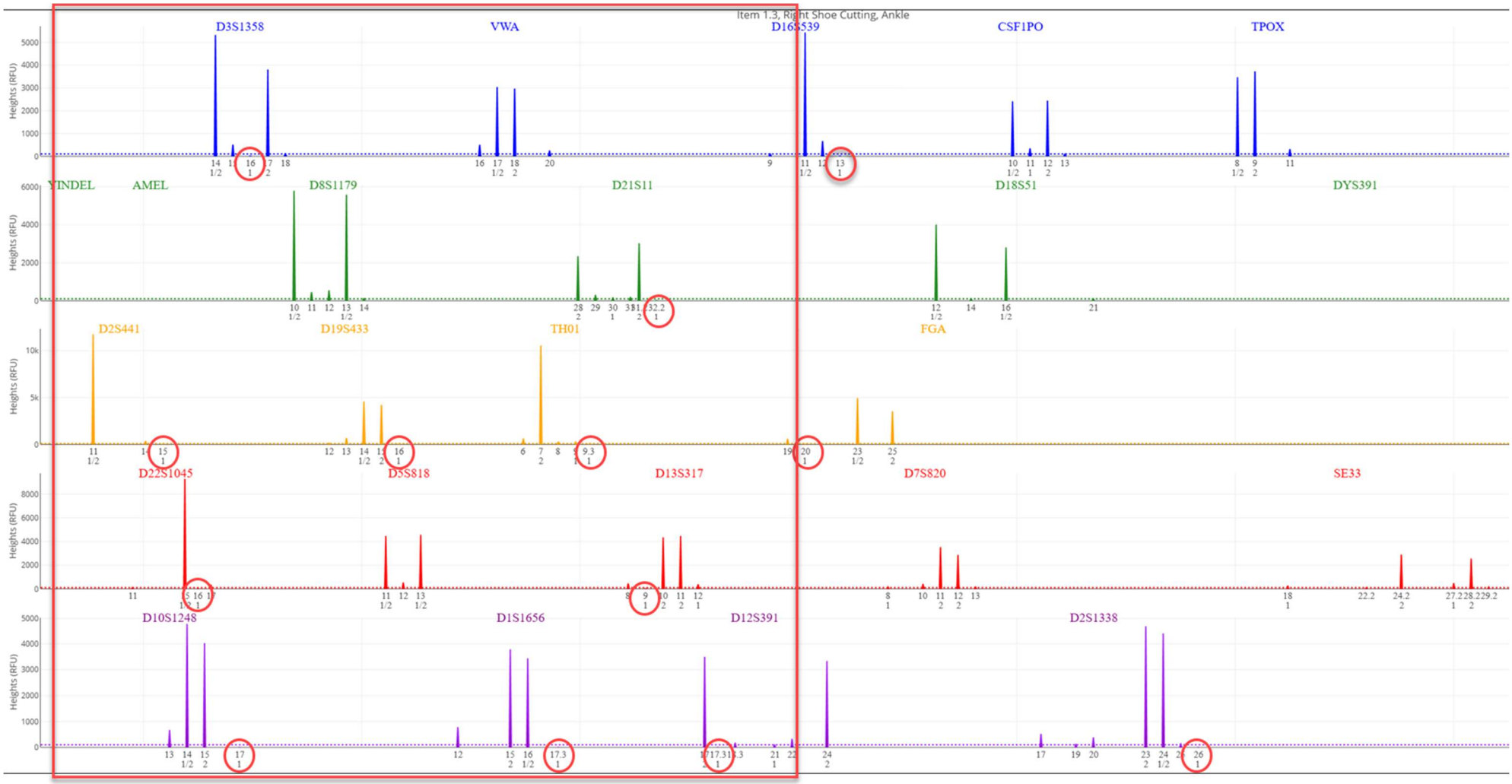

Item 1.3, Right Shoe Cutting, Ankle
D3S1358
VWA
D16S539
CSF1PO
TPOX
YINDEL
AMEL
D8S1179
D21S11
D18S51
DYS391
D2S441
D19S433
TH01
FGA
D22S1045
D5S818
D13S317
D7S820
SE33
D10S1248
D1S1656
D12S391
D2S1338
Heights (RFU)

Exhibit 4

00N-481 : 0555

STRMIX.
RESOLVE MORE DNA MIXTURES.

http://STRMIX.esr.cri.nz

Not Used. Upon further analysis, Number of Contr; Autors expanded to 4. → see EPG @ D21, D7, SE33, D12, D2

STRmix V2.4.05 - User:	jmoore
Advanced Report Version:	3.0.7
Analysis run:	08 September 2017 19:13
Time taken:	00:19:18.275
Case number:	00N-481
Sample ID:	x1-3
Comments:	

SUMMARY OF INPUT DATA

Kit Used	GlobalFiler_24
Number of Contributors	3
Input Files	26-00N-481-x1.3.csv
Known contributors under Hp	
Known contributors under Hd	

SUMMARY OF CONTRIBUTORS

Contributor	1	2	3
DNA Amounts	5156	251	127
Mixture Proportions	93%	5%	2%
Degradation starting at 84.0bp (rfu/bp)	7.929	0.401	0.184

RUN INFORMATION

Total iterations (Acceptance Rate)	1.0984063E7 (1 in 27.46)	**Gelman-Rubin convergence diagnostic**	1.08
Inter replicate efficiency	PCR 1 - 100.00%	**Allele variance (mode=8.811)**	7.80
Effective sample size	7257.51	**Stutter variance (mode=13.815)**	13.30
Average (log) likelihood	62.08	**Seed value**	610316
Mx prior mean	n/a	**Mx prior variance**	n/a

STUTTER FILES USED IN RUN

	File name
Stutter File	GF_stutter_OSP.txt
Stutter Exceptions File	GF_Stutter_Exceptions_OSP.csv
Forward Stutter File	GF_N+1_stutter_OSP.txt

Exhibit 5

STRmix V2.4.05 - User:	jmoore
Advanced Report Version:	3.0.7
Analysis run:	15 September 2017 17:55
Time taken:	00:54:05.471
Case number:	00N-481
Sample ID:	1-3
Comments:	Deconvolution with NOC = 4

SUMMARY OF INPUT DATA

Kit Used	GlobalFiler_24
Number of Contributors	4
Input Files	26-00N-481-x1.3.csv
Known contributors under Hp	
Known contributors under Hd	

SUMMARY OF CONTRIBUTORS

Contributor	1	2	3	4
DNA Amounts	5100	225	142	86
Mixture Proportions	92%	4%	3%	2%
Degradation starting at 84.0bp (rfu/bp)	8.308	0.456	0.248	0.162

RUN INFORMATION

Total iterations (Acceptance Rate)	2.557598E7 (1 in 63.94)	**Gelman-Rubin convergence diagnostic**	1.01
Inter replicate efficiency	PCR 1 - 100.00%	**Allele variance (mode=8.811)**	7.80
Effective sample size	5752.70	**Stutter variance (mode=13.815)**	11.20
Average (log) likelihood	60.39	**Seed value**	665332
Mx prior mean	n/a	**Mx prior variance**	n/a

STUTTER FILES USED IN RUN

	File name
Stutter File	GF_stutter_OSP.txt
Stutter Exceptions File	GF_Stutter_Exceptions_OSP.csv
Forward Stutter File	GF_N+1_stutter_OSP.txt

Exhibit 6

STRmix V2.4.05 - User:	jmoore
Advanced Report Version:	3.0.7
Analysis run:	25 September 2017 11:11
Time taken:	00:06:27.833
Case number:	00N-481
Sample ID:	x1-3
Comments:	4 Contrib, Condition on x4

SUMMARY OF INPUT DATA

Kit Used	GlobalFiler_24
Number of Contributors	4
Input Files	26-00N-481-x1.3.csv
Known contributors under Hp	27-00N-481-x4.csv
Known contributors under Hd	27-00N-481-x4.csv

SUMMARY OF CONTRIBUTORS

Contributor	1	2	3	4
DNA Amounts	5175	217	146	90
Mixture Proportions	92%	4%	3%	2%
Degradation starting at 84.0bp (rfu/bp)	8.511	0.487	0.270	0.173
Contributor Order giving highest LR	27-00N-481-x4.csv	Unknown	Unknown	Unknown

RUN INFORMATION

Total iterations (Acceptance Rate)	2.47862E7 (1 in 61.97)	**Gelman-Rubin convergence diagnostic**	1.07
Inter replicate efficiency	PCR 1 - 100.00%	**Allele variance (mode=8.811)**	7.70
Effective sample size	33795.04	**Stutter variance (mode=13.815)**	11.80
Average (log) likelihood	60.03	**Seed value**	270960
Mx prior mean	n/a	**Mx prior variance**	n/a

STUTTER FILES USED IN RUN

	File name
Stutter File	GF_stutter_OSP.txt
Stutter Exceptions File	GF_Stutter_Exceptions_OSP.csv
Forward Stutter File	GF_N+1_stutter_OSP.txt

Exhibit 7

7.8.8 Amendments to reports

7.8.8.1 When an issued report needs to be changed, amended or re-issued, any change of information shall be clearly identified and, where appropriate, the reason for the change included in the report.

7.8.8.2 Amendments to a report after issue shall be made only in the form of a further document, or data transfer, which includes the statement “Amendment to Report, serial number... [or as otherwise identified]”, or an equivalent form of wording.

Such amendments shall meet all the requirements of this document.

7.8.8.3 When it is necessary to issue a complete new report, this shall be uniquely identified and shall contain a reference to the original that it replaces